**Amendments to the Specification:**

Please replace the paragraph bridging pages 1-2 of the specification as follows:

The present invention relates to the identification of genes which are differentially expressed in transplant biopsies, e.g. renal biopsies, prior to the onset of CR in patients who will develop CR after the biopsy was taken, and patients that will not. The resulting gene expression pattern of a subset of the genes allows a highly statistically significant predictability of the occurrence of CR. For example, the genes identified in renal biopsies post transplantation before CR became histologically manifest, are indicated in Tables 1 (upregulated genes) and 2 (downregulated genes) and a subset of preferred genes in Table 3. The complete sequences of these 65 genes disclosed in this application are available using the ~~GenBank~~ GENBANK® accession number shown in Tables 1 to 3. The sequences as shown under the corresponding ~~GenBank~~ GENBANK® accession number are incorporated herein by reference.

Please replace the fourth full paragraph of page 2 of the specification as follows:

In a further embodiment, the levels of the gene expression products (proteins) can be monitored in various body fluids, including, but not limited to, blood plasma, serum, lymph, urine, stool and bile, or in biopsy tissues. This expression product level can be used as surrogate markers for early diagnosis of CR and can provide indices of therapy responsiveness. An example is e.g. the protein encoded by the Connective Tissue Growth Factor (~~GenBank~~ GENBANK® accession number X78947).

Please replace the first paragraph on page 8 of the specification as follows:

Gene expression profiles can be generated using e.g. the Affymetrix microarray technology. Microarrays are known in the art and consist of a surface to which probes that correspond in sequence to gene products (e.g. mRNAs, polypeptides, fragments thereof etc.). can be specifically hybridized or bound to a known position. Hybridization intensity data detected by the

scanner are automatically acquired and processed by the ~~GeneChip~~ GENECHIP® software. Raw data is normalized to expression levels using a target intensity of 200.

Please replace the paragraph on page 10 under the heading "RNA Amplification" as follows:

Prior to the RNA amplification procedure, all RNA eluates are treated with ~~RNeasy~~ RNEASY® kit chemistry (Qiagen) to further clean the RNA from remnant salt or other substances that may inhibit the amplification efficiency. The volume of the aliquot is adjusted to 100 µl with RNase-free water. 350 µl buffer RLT is added and mixed thoroughly. 250 µl ethanol (96-100%) is added, and mixed thoroughly. The sample (700 µl) is applied to an ~~RNeasy~~ RNEASY® mini column, placed in a 2 ml collection tube. After a 15 second centrifugation step at more than 10,000 rpm, the flow-through is discarded. The ~~RNeasy~~ RNEASY® column is transferred into a new 2 ml collection tube. 500 µl buffer RPE is pipetted onto the column, the tube closed and centrifuged for 15 seconds at more than 10,000 rpm to wash the column. The flow-through is discarded. Another 500 µl buffer RPE is added to the column and the tube is centrifuged for 2 minutes at more than 10,000 rpm to dry the silica-gel membrane. To elute, the ~~RNeasy~~ RNEASY® column is transferred to a new 1,5 ml collection tube and 30 µl RNase-free water is added directly onto the membrane. After 1 minute incubation, the tube is centrifuged for 1 minute at more than 10,000 rpm to elute. This elution step is repeated once to get a total elution volume of 60 µl. The RNA is quantified by the ~~Ribogreen~~ RIBOGREEN® method (Molecular Probes, Inc, USA). About 10 ng total RNA of each sample is used in three rounds of RNA amplification.